

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: December 13, 2002, 22:03:23 ; Search time 82 Seconds
(without alignments)
135.690 Million cell updates/sec

Title: US-09-659-737A-2
Perfect score: 293
Sequence: 1 HRDIKAGNILLLEKTEHDDI.....EWHRTTKMSTAGTYAMWAP 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	282	96.2	564	4	Q9H1Y7 homo sapien
2	278	94.9	570	4	Q8WNN2 homo sapien
3	278	94.9	1036	4	Q8WNN1 homo sapien
4	274	93.5	1001	11	Q8VDG6 mus musculu
5	239	81.6	69	11	Q9QVQ5 mus sp. pro
6	239	81.6	1066	4	Q9H2N5 mus musculu
7	231	78.8	847	4	Q16584 homo sapien
8	230	78.5	850	11	Q9QV15 mus musculu
9	216	73.7	69	11	Q9QVQ4 mus sp. pro
10	184	62.8	1020	5	Q9W313 drosophila
11	184	62.8	1148	5	Q9SVF6 drosophila
12	184	62.8	1161	5	Q95UN8 drosophila
13	139.5	47.6	977	5	Q9W24 drosophila
14	127	43.3	356	10	Q9LZM1 arabidopsis
15	124.5	42.5	859	4	Q8WY25 homo sapien
16	122	41.6	346	10	Q9FGS7 arabidopsis

17	121.5	41.5	111	4	Q15450 homo sapien
18	121.5	41.5	966	4	Q43283 homo sapien
19	121	41.3	356	10	Q39029 arabidopsis
20	121	41.3	356	10	Q9L756 arabidopsis
21	121	41.3	978	5	Q8T721 caenorhabd1
22	121	41.3	1040	5	Q8T720 caenorhabd1
23	117	39.9	957	10	Q9FPR4 hordeum vul
24	114.5	39.1	545	10	Q9SZM7 arabidopsis
25	114	38.9	454	11	Q9ESL3 mus musculu
26	114	38.9	455	4	Q9HCC4 homo sapien
27	114	38.9	800	4	Q9HDD2 homo sapien
28	114	38.9	800	4	Q9HCC5 homo sapien
29	114	38.9	800	4	Q9NYL2 homo sapien
30	114	38.9	800	4	Q9NVE9 homo sapien
31	114	38.9	802	11	Q9ESL4 mus musculu
32	113.5	38.7	405	10	Q9LVO9 arabidopsis
33	113	38.6	353	10	Q9FM43 arabidopsis
34	113	38.6	371	13	Q902X8 arabidopsis
35	112.5	38.4	663	10	Q8RYH9 oryza sativ
36	111	37.9	406	10	Q23719 arabidopsis
37	111	37.9	880	10	Q8S9K4 arabidopsis
38	111	37.9	886	10	Q9LYT8 arabidopsis
39	111	37.9	1030	10	Q9C9U5 arabidopsis
40	110.5	37.7	1151	10	Q9S716 arabidopsis
41	110	37.5	773	10	Q9C9U2 arabidopsis
42	109	37.2	227	10	Q9AR69 rosa hybrid
43	108	36.9	671	10	Q9C547 arabidopsis
44	107.5	36.7	411	10	Q9ZQ31 arabidopsis
45	107.5	36.7	1338	3	Q60030 kluyveromyc

ALIGNMENTS

RESULT 1					
ID	Q9H1Y7	PRELIMINARY:	PRT:	564	AA.
AC	Q9H1Y7:				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	DJ862P8.3 (Similar to MAP3K10 (Mitogen-activated protein kinase kinase kinase 10)) (Fragment).				
DE	DJ862P8.3.				
GN	Homo sapiens (Human).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
FN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Hall R.;				
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.				
DR	EMBL: AL133380; CACT1571.1; -.				
DR	HSSP: P06241; ISHF.				
DR	InterPro: IPR000719; Euk_pkinase.				
DR	InterPro: IPR002290; Ser_thr_pkinase.				
DR	InterPro: IPR001452; SH3.				
DR	InterPro: IPR001245; Tyr_pkinase.				
DR	Pfam: PF00069; pkinase.1.				
DR	Pfam: PF00018; SH3.1.				
DR	PRINTS: PR00452; SH3DOMAIN.				
DR	PRINTS: PR00109; TYRKINASE.				
DR	ProDom: PD000001; Euk_pkinase.1.				
DR	ProDom: PD000066; SH3.1.				
DR	SMART: SM00326; SH3.1.				
DR	SMART: SM00220; S_TKC.1.				
DR	SMART: SM00219; TYTK.1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.				
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM.1.				
DR	PROSITE: PS00108; PROTEIN_KINASE_ST.1.				
DR	PROSITE: PS50002; SH3.1.				
KW	kinase; SH3 domain.				

[illegible][illegible]

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DR PROSITE: PS50002; SH3; 1.  
KW ATP-binding; Kinase; SH3 domain; Serine/threonine-protein kinase;  
KW Transferase.  
SQ SEQUENCE 847 AA; 92687 MW; AFB6E930EA281C15 CRC64;  
  
Query Match 78.8%; Score 231; DB 4; Length 847;  
Best Local Similarity 77.8%; Pred. No. 1.2e-21;  
Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
  
OY 1 HRDIRKGNILILEKIEHDDICNKTITDPGLAREHWRRTTKMSTAGTYAMMAPE 54  
DB 239 HRDLKSNILLIPIETSDMEHRTKLTIDPGLAREHWRRTTKMSAAGTYAMMAPE 292  
  
RESULT 8  
O9JUI5 PRELIMINARY; PRT; 850 AA.  
AC O9JUI5; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Mixed lineage kinase 3.  
GN MLK3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/OLA;  
RA MEDLINE=20354997; PubMed=10894943;  
RA Saridadi A., Ferraz C., Demaille J., Scherer G., Roux A.-F.;  
RT "Genomic sequencing reveals the structure of the Kcnk6 and Mep3k11  
RT genes and their close vicinity to the Sipa1 gene on mouse chromosome  
RT 19.";  
RL Cytogenet. Cell Genet. 89:85-88(2000).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
DR EMBL; AF151142; AAF73281.1; -.  
DR HSSP; P29355; 1SEM.  
DR InterPro: IPR000719; Euk_pkinase.  
DR InterPro: IPR002290; Ser_thr_pkinase.  
DR InterPro: IPR001452; SH3.  
DR InterPro: IPR001245; Tyr_pkinase.  
DR Pfam; PF000069; pkinase; 1.  
DR Pfam; PF00018; SH3; 1.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Euk_pkinase; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR SMART; SM00219; Tyrc; 1.  
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.  
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.  
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.  
DR PROSITE; PS50002; SH3; 1.  
KW ATP-binding; Kinase; SH3 domain; Serine/threonine-protein kinase;  
KW Transferase.  
SQ SEQUENCE 850 AA; 93199 MW; 8F026CB3532DC10E CRC64;  
  
Query Match 78.5%; Score 230; DB 11; Length 850;  
Best Local Similarity 77.8%; Pred. No. 1.6e-21;  
Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
  
OY 1 HRDIFAGNILLLEKIEHDDICNKTITDPGLAREHWRRTTKMSTAGTYAMMAPE 54  
DB 240 HRDLKSNILLIPIETSDMEHRTKLTIDPGLAREHWRRTTKMSAAGTYAMMAPE 293  
  
RESULT 9  
O9VOV4 PRELIMINARY; PRT; 69 AA.  
ID O9VOV4  
AC O9VOV4;
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DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Protein tyrosine-serine/threonine kinase (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96043742; PubMed=7591219;  
RA Andres A.C., Zuercher G., Djonov V., Flueck M., Ziemiecki A.;  
RT "Protein tyrosine kinase expression during the estrous cycle and  
RT carcinogenesis of the mammary gland.";  
RL Int. J. Cancer 63:288-296(1995).  
DR InterPro: IPR000719; Euk_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk_pkinase; 1.  
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.  
SQ SEQUENCE 69 AA; 7842 MW; BF3CF8A7604EBB3E CRC64;  
  
Query Match 73.7%; Score 216; DB 11; Length 69;  
Best Local Similarity 72.2%; Pred. No. 6.5e-21;  
Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
  
OY 1 HRDIFAGNILLLEKIEHDDICNKTITDPGLAREHWRRTTKMSTAGTYAMMAPE 54  
DB 1 HRDLKSNILLIPIETSDMEHRTKLTIDPGLAREHWRRTTKMSAAGTYAMMAPE 292  
  
RESULT 10  
O9W3I3 PRELIMINARY; PRT; 1020 AA.  
AC O9W3I3; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE CG2272 protein.  
GN MLK2 OR CG2272.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OX Ephydroidea; Drosophilidae; Drosophila.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RA MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H.C., Blake J.R.G., Chame M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Durbin K.J., Evans J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston R.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Modarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Moodage T., Morley K.C., Mu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AE003443: AAF46344.1: -.
DR HSP: P11362: IFGK.
DR FLYBase: FBgn0030018: MK2.
DR InterPro: IPR000719: Euk_pkinase.
DR InterPro: IPR002290: Ser_thr_pkinase.
DR InterPro: IPR001452: SH3.
DR InterPro: IPR004040: SH3_pkinase.
DR InterPro: IPR001245: Tyr_pkinase.
DR Pfam: PF00069: pkinase; 1.
DR PRINTS: PR00452: SH3DOMAIN.
DR PRINTS: PR00109: TYRKINASE.
DR ProDom: PD000001: Euk_pkinase; 1.
DR ProDom: PD000066: SH3; 1.
DR SMART: SM00326: SH3; 1.
DR SMART: SM00221: STYK; 1.
DR PROSITE: PS50011: PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108: PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50002: SH3; 1.
DR ATP-binding: SH3 domain; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1020 AA; 113701 MW; D48FD89C639A08F CRC64;

Query Match
Best Local Similarity 62.8%; Score 184; DB 5; Length 1020;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 HRDIAAGNILLLEKTEHDDICKTKITDIFGLAREMHRRTKSTAGTYAMAPE 54
Db 249 HRDLKSSNVLIYEALIEGNHLQOKTKITDIFGLAREMYNTQRMSAAGTYAMAPE 302

RESULT 11
Q95VF6 PRELIMINARY; PRT; 1148 AA.
AC Q95VF6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mixed lineage kinase.
GN MK2 OR DMLK OR CG2272.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NM NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Satyanarayanan P., Tzivion G., Barthwal M.K., Rana A.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF416233: AAL08011.1: -.
DR FLYBase: FBgn0030018: MK2.
DR InterPro: IPR000719: Euk_pkinase.
DR InterPro: IPR002290: Ser_thr_pkinase.
DR InterPro: IPR001452: SH3.
DR Pfam: PF00069: pkinase; 1.
DR Pfam: PF00018: SH3; 1.
DR ProDom: PD000001: Euk_pkinase; 1.
DR ProDom: PD000066: SH3; 1.
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DR PROSITE: PS50011: PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108: PROTEIN_KINASE_ST; UNKNOWN_1.
DR PROSITE: PS50002: SH3; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 1148 AA; 127511 MW; 66A7D7A6E75E116C CRC64;

Query Match
Best Local Similarity 62.8%; Score 184; DB 5; Length 1148;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 HRDIAAGNILLLEKTEHDDICKTKITDIFGLAREMHRRTKSTAGTYAMAPE 54
Db 249 HRDLKSSNVLIYEALIEGNHLQOKTKITDIFGLAREMYNTQRMSAAGTYAMAPE 302

RESULT 12
Q95UN8 PRELIMINARY; PRT; 1161 AA.
AC Q95UN8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Mixed lineage protein kinase.
GN MK2 OR SLPR OR CG2272.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NM NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEAD;
RA Stronach B.E., Perrimon N.;
RT "Activation of the JNK pathway during dorsal closure in Drosophila
RT requires the mixed lineage kinase, Slipper.";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY045717: AAK98795.1: -.
DR FLYBase: FBgn0030018: MK2.
DR InterPro: IPR000719: Euk_pkinase.
DR InterPro: IPR002290: Ser_thr_pkinase.
DR InterPro: IPR001452: SH3.
DR Pfam: PF00069: pkinase; 1.
DR Pfam: PF00018: SH3; 1.
DR ProDom: PD000001: Euk_pkinase; 1.
DR ProDom: PD000066: SH3; 1.
DR PROSITE: PS50011: PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108: PROTEIN_KINASE_ST; UNKNOWN_1.
DR PROSITE: PS50002: SH3; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 1161 AA; 128960 MW; DD6C7ABAC08EDA24 CRC64;

Query Match
Best Local Similarity 63.0%; Score 184; DB 5; Length 1161;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 HRDIAAGNILLLEKTEHDDICKTKITDIFGLAREMHRRTKSTAGTYAMAPE 54
Db 262 HRDLKSSNVLIYEALIEGNHLQOKTKITDIFGLAREMYNTQRMSAAGTYAMAPE 315

RESULT 13
Q9VW24 PRELIMINARY; PRT; 977 AA.
AC Q9VW24;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG8789 protein (LD14856p).
GN CG8789.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731137;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fester C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reineert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Styrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fise E.,
 RA George R., Gonzalez M., Guartin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AY094787; AAF49129.1; -;
 DR EMBL: AY094787; AAM11440.1; -;
 DR HSSP: P08631; IAD5.
 DR FlyBase: Fgn0036896; CG8789.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50010; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 977 AA; 109567 MW; 5CD235939C14D4E CRC64;

Query Match 47.6%; Score 139.5; DB 5; Length 977;
 Best Local Similarity 52.7%; Pred. No. 1.5e-09;

Matches 29; Conservative 9; Mismatches 8; Indels 9; Gaps 2;
 QY 1 HRDIKAGNIIILEKTEHDDICNKTITDGLAREWRTTKMSA-GTYANMAPE 54
 DB 270 HRDIKSPNII-----STNEVVKISDFGTSREWEISYTKMSFAGTYANMAPE 316
 RESULT 14
 09LZW1 PRELIMINARY; PRT; 356 AA.
 AC 09LZW1;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Protein kinase ATN1-like protein.
 GN T20L15_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,
 RA de Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarroel R., Gielens J., Van Montagu M., Bancroft I., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AL162351; CAB82755.1; -;
 DR HSSP: P08631; IAD5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS50017; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 356 AA; 40147 MW; 43AFD079FBF0B5BC CRC64;

Query Match 43.3%; Score 127; DB 10; Length 356;
 Best Local Similarity 51.8%; Pred. No. 2.1e-08;
 Matches 29; Conservative 7; Mismatches 10; Indels 10; Gaps 3;

QY 1 HRDIKAGNIIILEKTEHDDICNKTITDGLAREWRTTKMSA-GTYANMAPE 54
 DB 164 HRDIKPNLIIETN-----HKSVKLADGLARE-BSVETMPTAETGTVMMAPE 211
 RESULT 15
 08WY25 PRELIMINARY; PRT; 859 AA.
 AC 08WY25;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Zipper protein kinase.
 GN MAP3K12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

